

SEQUENCE LISTING

<110> NIPPON SHOKUBAI CO., LTD.

NATIONAL INSTITUTE OF TECHNOLOGY AND EVALUATION

<120> Novel Modified S-Hydroxynitrile lyase

<130> PH-2387-PCT

<140>

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<150> JP 2004-105642

<151> 2004-03-31

<160> 44

<170> PatentIn Ver. 2.1

<210> 1

<211> 777

<212> DNA

<213> Manihot esculenta

<220>

<223> Inventor: Ichige, Eita; Semba, Hisashi; Shijuku, Toshiaki; Harayama, Shigeaki

<220>

<221> CDS

<222> (1)..(777)

<400> 1

atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca 48

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala

1

5

10

15

tgg att tgg cac aaa ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa 96

Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys

20

25

30

gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att 144

Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile

35

40

45

gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc 192

Glu	Gln	Ile	Asn	Ser	Phe	Asp	Glu	Tyr	Ser	Glu	Pro	Leu	Leu	Thr	Phe		
50						55				60							
ctg	gaa	aaa	ctg	ccg	caa	ggc	gaa	aag	gtt	atc	att	gtt	ggt	gaa	agc	240	
Leu	Glu	Lys	Leu	Pro	Gln	Gly	Glu	Lys	Val	Ile	Ile	Val	Gly	Glu	Ser		
65					70				75						80		
tgt	gca	ggc	ctg	aac	att	gct	att	gct	gct	gat	cgt	tac	gtt	gac	aaa	288	
Cys	Ala	Gly	Leu	Asn	Ile	Ala	Ile	Ala	Ala	Asp	Arg	Tyr	Val	Asp	Lys		
				85					90						95		
att	gca	gct	ggc	gtt	ttc	cac	aac	tcc	ctg	ctg	ccg	gac	acc	gtt	cac	336	
Ile	Ala	Ala	Gly	Val	Phe	His	Asn	Ser	Leu	Leu	Pro	Asp	Thr	Val	His		
			100						105					110			
agc	ccg	tct	tac	act	gtt	gaa	aag	ctg	ctg	gaa	tcg	ttc	ccg	gac	tgg	384	
Ser	Pro	Ser	Tyr	Thr	Val	Glu	Lys	Leu	Leu	Glu	Ser	Phe	Pro	Asp	Trp		
			115					120						125			
cgt	gac	aca	gaa	tat	ttc	acg	ttc	acc	aac	atc	act	ggc	gaa	acc	atc	432	
Arg	Asp	Thr	Glu	Tyr	Phe	Thr	Phe	Thr	Asn	Ile	Thr	Gly	Glu	Thr	Ile		
			130					135						140			
act	acc	atg	aaa	ctg	ggc	ttc	gtt	ctg	ctg	cgt	gaa	aac	ctg	ttc	acc	480	
Thr	Thr	Met	Lys	Leu	Gly	Phe	Val	Leu	Leu	Arg	Glu	Asn	Leu	Phe	Thr		
145						150				155					160		
aaa	tgc	act	gat	ggc	gaa	tat	gaa	ctg	gca	aaa	atg	gtt	atg	cgc	aag	528	
Lys	Cys	Thr	Asp	Gly	Glu	Tyr	Glu	Leu	Ala	Lys	Met	Val	Met	Arg	Lys		
				165					170						175		
ggc	tct	ctg	ttc	caa	aac	gtt	ctg	gct	cag	cgt	ccg	aag	ttc	act	gaa	576	
Gly	Ser	Leu	Phe	Gln	Asn	Val	Leu	Ala	Gln	Arg	Pro	Lys	Phe	Thr	Glu		
				180					185						190		
aaa	ggc	tac	ggc	tct	atc	aag	aaa	gtt	tat	att	tgg	acc	gat	caa	gac	624	
Lys	Gly	Tyr	Gly	Ser	Ile	Lys	Lys	Val	Tyr	Ile	Trp	Thr	Asp	Gln	Asp		
				195					200					205			
aaa	ata	ttc	ctg	ccg	gac	ttc	caa	cgc	tgg	caa	att	gca	aac	tac	aaa	672	
Lys	Ile	Phe	Leu	Pro	Asp	Phe	Gln	Arg	Trp	Gln	Ile	Ala	Asn	Tyr	Lys		
				210					215					220			
ccg	gac	aag	gtt	tat	cag	gtt	caa	ggc	ggc	gat	cac	aag	ctg	cag	ctg	720	
Pro	Asp	Lys	Val	Tyr	Gln	Val	Gln	Gly	Gly	Asp	His	Lys	Leu	Gln	Leu		

225 230 235 240

aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca 768
 Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala
 245 250 255 ~

tac gct taa 777
 Tyr Ala

<210> 2
 <211> 258
 <212> PRT
 <213> Manihot esculenta

<400> 2
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 1 5 10 15
 Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys
 20 25 30
 Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile
 35 40 45
 Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe
 50 55 60
 Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser
 65 70 75 80
 Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys
 85 90 95
 Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His
 100 105 110
 Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp
 115 120 125
 Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile
 130 135 140
 Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr
 145 150 155 160
 Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys
 165 170 175
 Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu
 180 185 190
 Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp
 195 200 205
 Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys
 210 215 220
 Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu

225 230 235 240
 Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala
 245 250 255
 Tyr Ala

<210> 3
 <211> 774
 <212> DNA
 <213> Hevea brasiliensis

<220>
 <221> CDS
 <222> (1)..(774)

<400> 3
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 Met Ala Phe Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala
 1 5 10 15

 tgg att tgg cac aag ctc aaa ccc ctc ctt gag gca ctt ggc cac aag 96
 Trp Ile Trp His Lys Leu Lys Pro Leu Leu Glu Ala Leu Gly His Lys
 20 25 30

 gtt act gca ctg gac ctt gca gca agc ggc gtt gac cca agg caa att 144
 Val Thr Ala Leu Asp Leu Ala Ala Ser Gly Val Asp Pro Arg Gln Ile
 35 40 45

 gag gag att ggc tca ttt gat gag tat tct gaa ccc ttg ttg acg ttc 192
 Glu Glu Ile Gly Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe
 50 55 60

 ttg gag gca ctc cct cca ggg gaa aag gtg att ctg gtt ggc gag agc 240
 Leu Glu Ala Leu Pro Pro Gly Glu Lys Val Ile Leu Val Gly Glu Ser
 65 70 75 80

 tgt gga gga ctc aat ata gca att gct gct gat aaa tac tgt gaa aag 288
 Cys Gly Gly Leu Asn Ile Ala Ile Ala Ala Asp Lys Tyr Cys Glu Lys
 85 90 95

 att gca gct gct gtt ttc cac aat tca gta ttg cca gac acc gag cac 336
 Ile Ala Ala Ala Val Phe His Asn Ser Val Leu Pro Asp Thr Glu His
 100 105 110

tgc cca tct tac gtc gtg gat aag ctc atg gag gtg ttt ccc gac tgg 384
 Cys Pro Ser Tyr Val Val Asp Lys Leu Met Glu Val Phe Pro Asp Trp
 115 120 125

aaa gac acc acg tat ttt acg tac act aaa gat ggc aag gag ata-act 432
 Lys Asp Thr Thr Tyr Phe Thr Tyr Thr Lys Asp Gly Lys Glu Ile Thr
 130 135 140

gga ttg aaa ctg ggc ttc acg ctt ctg agg gaa aat tta tat acc ctt 480
 Gly Leu Lys Leu Gly Phe Thr Leu Leu Arg Glu Asn Leu Tyr Thr Leu
 145 150 155 160

tgc ggt cct gag gaa tat gaa ctg gcg aag atg ttg aca agg aag gga 528
 Cys Gly Pro Glu Glu Tyr Glu Leu Ala Lys Met Leu Thr Arg Lys Gly
 165 170 175

tca tta ttt caa aat att tta gct aag cga cca ttc ttc act aag gaa 576
 Ser Leu Phe Gln Asn Ile Leu Ala Lys Arg Pro Phe Phe Thr Lys Glu
 180 185 190

ggt tac gga tcg att aag aaa att tat gtg tgg acc gac caa gac gaa 624
 Gly Tyr Gly Ser Ile Lys Lys Ile Tyr Val Trp Thr Asp Gln Asp Glu
 195 200 205

ata ttt tta cct gaa ttt caa ctc tgg caa ata gaa aac tat aaa cca 672
 Ile Phe Leu Pro Glu Phe Gln Leu Trp Gln Ile Glu Asn Tyr Lys Pro
 210 215 220

gac aag gtt tat aag gtc gaa ggt gga gat cat aaa ttg cag ctt aca 720
 Asp Lys Val Tyr Lys Val Glu Gly Gly Asp His Lys Leu Gln Leu Thr
 225 230 235 240

aag act aag gag atc gct gaa att ctc caa gag gtg gct gat acc tat 768
 Lys Thr Lys Glu Ile Ala Glu Ile Leu Gln Glu Val Ala Asp Thr Tyr
 245 250 255

aat tga 774
 Asn

<210> 4

<211> 257

<212> PRT

<213> Hevea brasiliensis

<400> 4

Met Ala Phe Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala
 1 5 10 15
 Trp Ile Trp His Lys Leu Lys Pro Leu Leu Glu Ala Leu Gly His Lys
 20 25 30
 Val Thr Ala Leu Asp Leu Ala Ala Ser Gly Val Asp Pro Arg Gln Ile
 35 40 45
 Glu Glu Ile Gly Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe
 50 55 60
 Leu Glu Ala Leu Pro Pro Gly Glu Lys Val Ile Leu Val Gly Glu Ser
 65 70 75 80
 Cys Gly Gly Leu Asn Ile Ala Ile Ala Ala Asp Lys Tyr Cys Glu Lys
 85 90 95
 Ile Ala Ala Ala Val Phe His Asn Ser Val Leu Pro Asp Thr Glu His
 100 105 110
 Cys Pro Ser Tyr Val Val Asp Lys Leu Met Glu Val Phe Pro Asp Trp
 115 120 125
 Lys Asp Thr Thr Tyr Phe Thr Tyr Thr Lys Asp Gly Lys Glu Ile Thr
 130 135 140
 Gly Leu Lys Leu Gly Phe Thr Leu Leu Arg Glu Asn Leu Tyr Thr Leu
 145 150 155 160
 Cys Gly Pro Glu Glu Tyr Glu Leu Ala Lys Met Leu Thr Arg Lys Gly
 165 170 175
 Ser Leu Phe Gln Asn Ile Leu Ala Lys Arg Pro Phe Phe Thr Lys Glu
 180 185 190
 Gly Tyr Gly Ser Ile Lys Lys Ile Tyr Val Trp Thr Asp Gln Asp Glu
 195 200 205
 Ile Phe Leu Pro Glu Phe Gln Leu Trp Gln Ile Glu Asn Tyr Lys Pro
 210 215 220
 Asp Lys Val Tyr Lys Val Glu Gly Gly Asp His Lys Leu Gln Leu Thr
 225 230 235 240
 Lys Thr Lys Glu Ile Ala Glu Ile Leu Gln Glu Val Ala Asp Thr Tyr
 245 250 255
 Asn

<210> 5

<211> 777

<212> DNA

<213> Manihot esculenta

<220>

<223> cDNA coding for Modified SHNL involving
 a replacement of Gly by Asp at position 165

<220>

<221> CDS

<222> (1).. (777)

<400> 5

atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca	48
Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala	
1 5 10 15	
tgg att tgg cac aaa ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa	96
Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys	
20 25 30	
gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att	144
Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile	
35 40 45	
gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc	192
Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe	
50 55 60	
ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc	240
Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser	
65 70 75 80	
tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa	288
Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys	
85 90 95	
att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac	336
Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His	
100 105 110	
agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg	384
Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp	
115 120 125	
cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc	432
Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile	
130 135 140	
act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc acc	480
Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr	
145 150 155 160	

aaa tgc act gat gac gaa tat gaa ctg gca aaa atg gtt atg cgc aag 528
 Lys Cys Thr Asp Asp Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys
 165 170 175

ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa 576
 Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu
 180 185 190

aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac 624
 Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp
 195 200 205

aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa 672
 Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys
 210 215 220

ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg 720
 Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu
 225 230 235 240

aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca 768
 Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala
 245 250 255

tac gct taa 777
 Tyr Ala

<210> 6

<211> 258

<212> PRT

<213> Manihot esculenta

<220>

<223> Modified SHNL involving

a replacement of Gly by Asp at position 165

<400> 6

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala
 1 5 10 15
 Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys
 20 25 30
 Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile
 35 40 45

Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe
 50 55 60
 Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser
 65 70 75 80
 Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp-Lys
 85 90 95
 Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His
 100 105 110
 Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp
 115 120 125
 Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile
 130 135 140
 Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr
 145 150 155 160
 Lys Cys Thr Asp Asp Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys
 165 170 175
 Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu
 180 185 190
 Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp
 195 200 205
 Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys
 210 215 220
 Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu
 225 230 235 240
 Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala
 245 250 255
 Tyr Ala

<210> 7

<211> 777

<212> DNA

<213> Manihot esculenta

<220>

<221> CDS

<222> (1).. (777)

<220>

<223> cDNA coding for Modified SHNL involving
 a replacement of Gly by Glu at position 165

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1				5					10					15		
tgg	att	tgg	cac	aaa	ctg	aaa	ccg	gcc	ctg	gaa	cgt	gct	ggc	cac	aaa	96
Trp	Ile	Trp	His	Lys	Leu	Lys	Pro	Ala	Leu	Glu	Arg	Ala	Gly	His	Lys	
			20					25					30			
ggt	act	gca	ctg	gac	atg	gca	gcc	agt	ggc	att	gac	ccg	cgt	caa	att	144
Val	Thr	Ala	Leu	Asp	Met	Ala	Ala	Ser	Gly	Ile	Asp	Pro	Arg	Gln	Ile	
		35					40				45					
gaa	cag	atc	aac	tct	ttc	gat	gaa	tac	tct	gaa	ccg	ctg	ctg	act	ttc	192
Glu	Gln	Ile	Asn	Ser	Phe	Asp	Glu	Tyr	Ser	Glu	Pro	Leu	Leu	Thr	Phe	
	50					55				60						
ctg	gaa	aaa	ctg	ccg	caa	ggc	gaa	aag	gtt	atc	att	gtt	ggt	gaa	agc	240
Leu	Glu	Lys	Leu	Pro	Gln	Gly	Glu	Lys	Val	Ile	Ile	Val	Gly	Glu	Ser	
65					70				75					80		
tgt	gca	ggc	ctg	aac	att	gct	att	gct	gct	gat	cgt	tac	gtt	gac	aaa	288
Cys	Ala	Gly	Leu	Asn	Ile	Ala	Ile	Ala	Ala	Asp	Arg	Tyr	Val	Asp	Lys	
				85				90					95			
att	gca	gct	ggc	gtt	ttc	cac	aac	tcc	ctg	ctg	ccg	gac	acc	gtt	cac	336
Ile	Ala	Ala	Gly	Val	Phe	His	Asn	Ser	Leu	Leu	Pro	Asp	Thr	Val	His	
			100					105				110				
agc	ccg	tct	tac	act	gtt	gaa	aag	ctg	ctg	gaa	tcg	ttc	ccg	gac	tgg	384
Ser	Pro	Ser	Tyr	Thr	Val	Glu	Lys	Leu	Leu	Glu	Ser	Phe	Pro	Asp	Trp	
		115					120					125				
cgt	gac	aca	gaa	tat	ttc	acg	ttc	acc	aac	atc	act	ggc	gaa	acc	atc	432
Arg	Asp	Thr	Glu	Tyr	Phe	Thr	Phe	Thr	Asn	Ile	Thr	Gly	Glu	Thr	Ile	
	130					135				140						
act	acc	atg	aaa	ctg	ggt	ttc	gtt	ctg	ctg	cgt	gaa	aac	ctg	ttc	acc	480
Thr	Thr	Met	Lys	Leu	Gly	Phe	Val	Leu	Leu	Arg	Glu	Asn	Leu	Phe	Thr	
145					150					155				160		
aaa	tgc	act	gat	gaa	gaa	tat	gaa	ctg	gca	aaa	atg	gtt	atg	cgc	aag	528
Lys	Cys	Thr	Asp	Glu	Glu	Tyr	Glu	Leu	Ala	Lys	Met	Val	Met	Arg	Lys	
				165				170					175			
ggc	tct	ctg	ttc	caa	aac	gtt	ctg	gct	cag	cgt	ccg	aag	ttc	act	gaa	576
Gly	Ser	Leu	Phe	Gln	Asn	Val	Leu	Ala	Gln	Arg	Pro	Lys	Phe	Thr	Glu	

180 185 190
 aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac 624
 Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp
 195 200 205
 aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa 672
 Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys
 210 215 220
 ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg 720
 Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu
 225 230 235 240
 aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca 768
 Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala
 245 250 255
 tac gct taa 777
 Tyr Ala

<210> 8

<211> 258

<212> PRT

<213> Manihot esculenta

<220>

<223> Modified SHNL involving

a replacement of Gly by Glu at position 165

<400> 8

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala
 1 5 10 15
 Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys
 20 25 30
 Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile
 35 40 45
 Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe
 50 55 60
 Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser
 65 70 75 80
 Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys
 85 90 95
 Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His

	100		105		110										
Ser	Pro	Ser	Tyr	Thr	Val	Glu	Lys	Leu	Leu	Glu	Ser	Phe	Pro	Asp	Trp
	115		120		125										
Arg	Asp	Thr	Glu	Tyr	Phe	Thr	Phe	Thr	Asn	Ile	Thr	Gly	Glu	Thr	Ile
	130		135		140										
Thr	Thr	Met	Lys	Leu	Gly	Phe	Val	Leu	Leu	Arg	Glu	Asn	Leu	Phe	Thr
145			150		155									160	
Lys	Cys	Thr	Asp	Glu	Glu	Tyr	Glu	Leu	Ala	Lys	Met	Val	Met	Arg	Lys
	165		170		175										
Gly	Ser	Leu	Phe	Gln	Asn	Val	Leu	Ala	Gln	Arg	Pro	Lys	Phe	Thr	Glu
	180		185		190										
Lys	Gly	Tyr	Gly	Ser	Ile	Lys	Lys	Val	Tyr	Ile	Trp	Thr	Asp	Gln	Asp
	195		200		205										
Lys	Ile	Phe	Leu	Pro	Asp	Phe	Gln	Arg	Trp	Gln	Ile	Ala	Asn	Tyr	Lys
	210		215		220										
Pro	Asp	Lys	Val	Tyr	Gln	Val	Gln	Gly	Gly	Asp	His	Lys	Leu	Gln	Leu
225			230		235									240	
Thr	Lys	Thr	Glu	Glu	Val	Ala	His	Ile	Leu	Gln	Glu	Val	Ala	Asp	Ala
	245		250		255										
Tyr	Ala														

<210> 9

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 9

ggggaattca tggttactgc acacttcggt ctgattcac

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<210> 10

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 10

gggaagcttt taagcgatg catcagcaac ttcttcgag

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<210> 11
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 11
gggggggggc atatggttac tgcacacttc gttctgattc acac 44

<210> 12
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 12
gggggatcct taagcgtatg catcagcaac ttcttgag 39

<210> 13
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 13
cgtgaaaacc tggtcaccaa atgcactgat gaagaatatg aactggcaaa aatg 54

<210> 14
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 14

catttttggcc agttcatatt cttcatcagt gcatttggtg aacagggtttt cacg

54

<210> 15

<211> 777

<212> DNA

<213> Manihot esculenta

<220>

<221> CDS

<222> (1)..(777)

<220>

<223> cDNA coding for Modified SHNL involving
a replacement of Val by Leu at position 173

<400> 15

atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca 48

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala

1 5 10 15

tgg att tgg cac aaa ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa 96

Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys

20 25 30

gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att 144

Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile

35 40 45

gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc 192

Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe

50 55 60

ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc 240

Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser

65 70 75 80

tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa 288

Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys

85 90 95

att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac 336

Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His

100	105	110	
agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg			384
Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp			
115	120	125	
cg t gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc			432
Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile			
130	135	140	
act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc acc			480
Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr			
145	150	155	160
aaa tgc act gat ggc gaa tat gaa ctg gca aaa atg ctg atg cgc aag			528
Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Leu Met Arg Lys			
165	170	175	
ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa			576
Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu			
180	185	190	
aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac			624
Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp			
195	200	205	
aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa			672
Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys			
210	215	220	
ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg			720
Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu			
225	230	235	240
aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca			768
Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala			
245	250	255	
tac gct taa			777
Tyr Ala			

<210> 16

<211> 258

<212> PRT

<213> Manihot esculenta

<220>

<223> Modified SHNL involving
a replacement of Val by Leu at position 173

<400> 16

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Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala
 1           5           10           15
Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys
      20           25           30
Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile
      35           40           45
Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe
      50           55           60
Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser
      65           70           75           80
Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys
      85           90           95
Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His
      100          105          110
Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp
      115          120          125
Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile
      130          135          140
Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr
      145          150          155          160
Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Leu Met Arg Lys
      165          170          175
Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu
      180          185          190
Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp
      195          200          205
Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys
      210          215          220
Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu
      225          230          235          240
Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala
      245          250          255
Tyr Ala

```

<210> 17

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 17

ggcgaatatg aactggcaaa aatgnnnatg cgcaagggt ctctg 45

<210> 18

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 18

cagagagccc ttgcgatnn ncatttttgc cagttcatat tcgcc 45

<210> 19

<211> 777

<212> DNA

<213> Manihot esculenta

<220>

<221> CDS

<222> (1)..(777)

<220>

<223> cDNA coding for Modified SHNL involving
a replacement of Met by Leu at position 174

<400> 19

atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca 48
Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala
1 5 10 15

tgg att tgg cac aaa ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa 96
Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys
20 25 30

gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att 144

Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile	
35 40 45	
gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc	192
Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe	
50 55 60	
ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc	240
Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser	
65 70 75 80	
tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa	288
Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys	
85 90 95	
att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac	336
Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His	
100 105 110	
agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg	384
Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp	
115 120 125	
cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc	432
Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile	
130 135 140	
act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc acc	480
Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr	
145 150 155 160	
aaa tgc act gat ggc gaa tat gaa ctg gca aaa atg gtt ttg cgc aag	528
Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Leu Arg Lys	
165 170 175	
ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa	576
Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu	
180 185 190	
aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac	624
Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp	
195 200 205	
aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa	672
Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys	

210 215 220

cgc gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg 720
 Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu
 225 230 235 ~240

aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca 768
 Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala
 245 250 255

tac gct taa 777
 Tyr Ala

<210> 20
 <211> 258
 <212> PRT
 <213> Manihot esculenta

<220>
 <223> Modified SHNL involving
 a replacement of Met by Leu at position 174

<400> 20
 Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala
 1 5 10 15
 Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys
 20 25 30
 Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile
 35 40 45
 Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe
 50 55 60
 Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser
 65 70 75 80
 Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys
 85 90 95
 Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His
 100 105 110
 Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp
 115 120 125
 Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile
 130 135 140
 Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr
 145 150 155 160
 Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Leu Arg Lys

```

                165                170                175
Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu
                180                185                190
Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp
                195                200                205
Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys
                210                215                220
Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu
225                230                235                240
Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala
                245                250                255
Tyr Ala

```

<210> 21
 <211> 777
 <212> DNA
 <213> *Manihot esculenta*

<220>
 <221> CDS
 <222> -(1)..(777)

<220>
 <223> cDNA coding for Modified SHNL(SHNL Actmt022-G12) involving
 a replacement of Lys by Asn at position 21

```

<400> 21
atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca 48
Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala
  1             5             10             15

tgg att tgg cac aat ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa 96
Trp Ile Trp His Asn Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys
      20             25             30

gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att 144
Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile
      35             40             45

gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc 192
Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe
      50             55             60

```

ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc 240
 Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser
 65 70 75 80

tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa 288
 Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys
 85 90 95

att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac 336
 Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His
 100 105 110

agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg 384
 Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp
 115 120 125

cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc 432
 Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile
 130 135 140

act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc acc 480
 Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr
 145 150 155 160

aaa tgc act gat ggc gaa tat gaa ctg gca aaa atg gtt atg cgc aag 528
 Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys
 165 170 175

ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa 576
 Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu
 180 185 190

aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac 624
 Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp
 195 200 205

aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa 672
 Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys
 210 215 220

ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg 720
 Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu
 225 230 235 240

aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca 768

Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala
 245 250 255

tac gct taa
 Tyr Ala

777

<210> 22
 <211> 258
 <212> PRT
 <213> Manihot esculenta

<220>
 <223> Modified SHNL(SHNL Actmt022-G12) involving
 a replacement of Lys by Asn at position 21

<400> 22
 Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala
 1 5 10 15
 Trp Ile Trp His Asn Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys
 20 25 30
 Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile
 35 40 45
 Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe
 50 55 60
 Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser
 65 70 75 80
 Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys
 85 90 95
 Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His
 100 105 110
 Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp
 115 120 125
 Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile
 130 135 140
 Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr
 145 150 155 160
 Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys
 165 170 175
 Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu
 180 185 190
 Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp
 195 200 205
 Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys
 210 215 220

Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu
 225 230 235 240
 Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala
 245 250 255
 Tyr Ala

<210> 23

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 23

ggcgcatgga ttggtcacnn nctgaaaccg gccctggaa

39

<210> 24

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 24

ttccagggcc ggtttcagnn ngtgccaaat ccatgcgcc

39

<210> 25

<211> 777

<212> DNA

<213> Manihot esculenta

<220>

<221> CDS

<222> (1)..(777)

<220>

<223> cDNA coding for Modified SHNL involving
 a replacement of Lys by Glu at position 21

<400> 25

atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca	48
Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala	
1 5 10 15	
tgg att tgg cac gaa ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa	96
Trp Ile Trp His Glu Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys	
20 25 30	
gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att	144
Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile	
35 40 45	
gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc	192
Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe	
50 55 60	
ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc	240
Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser	
65 70 75 80	
tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa	288
Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys	
85 90 95	
att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac	336
Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His	
100 105 110	
agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg	384
Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp	
115 120 125	
cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc	432
Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile	
130 135 140	
act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc acc	480
Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr	
145 150 155 160	
aaa tgc act gat ggc gaa tat gaa ctg gca aaa atg gtt atg cgc aag	528
Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys	
165 170 175	

ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa 576
 Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu
 180 185 190

aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac 624
 Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp
 195 200 205

aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa 672
 Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys
 210 215 220

ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg 720
 Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu
 225 230 235 240

aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca 768
 Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala
 245 250 255

tac gct taa 777
 Tyr Ala

<210> 26

<211> 258

<212> PRT

<213> Manihot esculenta

<220>

<223> Modified SHNL involving

a replacement of Lys by Glu at position 21

<400> 26

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala
 1 5 10 15
 Trp Ile Trp His Glu Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys
 20 25 30
 Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile
 35 40 45
 Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe
 50 55 60
 Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser
 65 70 75 80
 Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys

	85		90		95										
Ile	Ala	Ala	Gly	Val	Phe	His	Asn	Ser	Leu	Leu	Pro	Asp	Thr	Val	His
	100						105					110			
Ser	Pro	Ser	Tyr	Thr	Val	Glu	Lys	Leu	Leu	Glu	Ser	Phe	Pro	Asp	Trp
	115						120					125			
Arg	Asp	Thr	Glu	Tyr	Phe	Thr	Phe	Thr	Asn	Ile	Thr	Gly	Glu	Thr	Ile
	130					135					140				
Thr	Thr	Met	Lys	Leu	Gly	Phe	Val	Leu	Leu	Arg	Glu	Asn	Leu	Phe	Thr
145					150					155				160	
Lys	Cys	Thr	Asp	Gly	Glu	Tyr	Glu	Leu	Ala	Lys	Met	Val	Met	Arg	Lys
		165							170					175	
Gly	Ser	Leu	Phe	Gln	Asn	Val	Leu	Ala	Gln	Arg	Pro	Lys	Phe	Thr	Glu
	180						185					190			
Lys	Gly	Tyr	Gly	Ser	Ile	Lys	Lys	Val	Tyr	Ile	Trp	Thr	Asp	Gln	Asp
	195					200						205			
Lys	Ile	Phe	Leu	Pro	Asp	Phe	Gln	Arg	Trp	Gln	Ile	Ala	Asn	Tyr	Lys
210					215					220					
Pro	Asp	Lys	Val	Tyr	Gln	Val	Gln	Gly	Gly	Asp	His	Lys	Leu	Gln	Leu
225					230					235				240	
Thr	Lys	Thr	Glu	Glu	Val	Ala	His	Ile	Leu	Gln	Glu	Val	Ala	Asp	Ala
		245							250					255	

Tyr Ala

<210> 27

<211> 777

<212> DNA

<213> Manihot esculenta

<220>

<221> CDS

<222> (1)..(777)

<220>

<223> cDNA coding for Modified SHNL involving
a replacement of Lys by Asp at position 21

<400> 27

atg	gtt	act	gca	cac	ttc	gtt	ctg	att	ca	acc	att	tgt	cac	ggc	gca	48
Met	Val	Thr	Ala	His	Phe	Val	Leu	Ile	His	Thr	Ile	Cys	His	Gly	Ala	
1				5				10						15		

tgg	att	tgg	cac	gac	ctg	aaa	ccg	gcc	ctg	gaa	cgt	gct	ggc	cac	aaa	96
Trp	Ile	Trp	His	Asp	Leu	Lys	Pro	Ala	Leu	Glu	Arg	Ala	Gly	His	Lys	

20	25	30	
gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att			144
Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile			
35	40	45	
gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc			192
Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe			
50	55	60	
ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc			240
Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser			
65	70	75	80
tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa			288
Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys			
85	90	95	
att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac			336
Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His			
100	105	110	
agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg			384
Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp			
115	120	125	
cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc			432
Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile			
130	135	140	
act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc acc			480
Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr			
145	150	155	160
aaa tgc act gat ggc gaa tat gaa ctg gca aaa atg gtt atg cgc aag			528
Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys			
165	170	175	
ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa			576
Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu			
180	185	190	
aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac			624
Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp			
195	200	205	

aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa 672
 Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys
 210 215 220

ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg 720
 Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu
 225 230 235 240

aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca 768
 Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala
 245 250 255

tac gct taa 777
 Tyr Ala

<210> 28
 <211> 258
 <212> PRT
 <213> Manihot esculenta

<220>
 <223> Modified SHNL involving
 a replacement of Lys by Asp at position 21

<400> 28
 Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala
 1 5 10 15
 Trp Ile Trp His Asp Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys
 20 25 30
 Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile
 35 40 45
 Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe
 50 55 60
 Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser
 65 70 75 80
 Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys
 85 90 95
 Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His
 100 105 110
 Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp
 115 120 125
 Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile
 130 135 140

Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr
 145 150 155 160
 Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys
 165 170 175
 Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu
 180 185 190
 Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp
 195 200 205
 Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys
 210 215 220
 Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu
 225 230 235 240
 Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala
 245 250 255
 Tyr Ala

<210> 29

<211> 777

<212> DNA

<213> Manihot esculenta

<220>

<221> CDS

<222> (1).. (777)

<220>

<223> cDNA coding for Modified SHNL involving
 a replacement of Lys by Asn at position 21

<400> 29

atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca 48
 Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala
 1 5 10 15

tgg att tgg cac aac ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa 96
 Trp Ile Trp His Asn Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys
 20 25 30

gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att 144
 Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile
 35 40 45

gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc 192

Glu	Gln	Ile	Asn	Ser	Phe	Asp	Glu	Tyr	Ser	Glu	Pro	Leu	Leu	Thr	Phe		
50						55					60						
ctg	gaa	aaa	ctg	ccg	caa	ggc	gaa	aag	gtt	atc	att	gtt	ggt	gaa	agc	240	
Leu	Glu	Lys	Leu	Pro	Gln	Gly	Glu	Lys	Val	Ile	Ile	Val	Gly	Glu	Ser		
65					70				75						80		
tgt	gca	ggc	ctg	aac	att	gct	att	gct	gct	gat	cgt	tac	gtt	gac	aaa	288	
Cys	Ala	Gly	Leu	Asn	Ile	Ala	Ile	Ala	Ala	Asp	Arg	Tyr	Val	Asp	Lys		
				85				90						95			
att	gca	gct	ggc	gtt	ttc	cac	aac	tcc	ctg	ctg	ccg	gac	acc	gtt	cac	336	
Ile	Ala	Ala	Gly	Val	Phe	His	Asn	Ser	Leu	Leu	Pro	Asp	Thr	Val	His		
			100					105					110				
agc	ccg	tct	tac	act	gtt	gaa	aag	ctg	ctg	gaa	tcg	ttc	ccg	gac	tgg	384	
Ser	Pro	Ser	Tyr	Thr	Val	Glu	Lys	Leu	Leu	Glu	Ser	Phe	Pro	Asp	Trp		
		115					120				125						
cgt	gac	aca	gaa	tat	ttc	acg	ttc	acc	aac	atc	act	ggc	gaa	acc	atc	432	
Arg	Asp	Thr	Glu	Tyr	Phe	Thr	Phe	Thr	Asn	Ile	Thr	Gly	Glu	Thr	Ile		
	130					135				140							
act	acc	atg	aaa	ctg	ggc	ttc	gtt	ctg	ctg	cgt	gaa	aac	ctg	ttc	acc	480	
Thr	Thr	Met	Lys	Leu	Gly	Phe	Val	Leu	Leu	Arg	Glu	Asn	Leu	Phe	Thr		
145					150				155					160			
aaa	tgc	act	gat	ggc	gaa	tat	gaa	ctg	gca	aaa	atg	gtt	atg	cgc	aag	528	
Lys	Cys	Thr	Asp	Gly	Glu	Tyr	Glu	Leu	Ala	Lys	Met	Val	Met	Arg	Lys		
				165				170						175			
ggc	tct	ctg	ttc	caa	aac	gtt	ctg	gct	cag	cgt	ccg	aag	ttc	act	gaa	576	
Gly	Ser	Leu	Phe	Gln	Asn	Val	Leu	Ala	Gln	Arg	Pro	Lys	Phe	Thr	Glu		
			180					185					190				
aaa	ggc	tac	ggc	tct	atc	aag	aaa	gtt	tat	att	tgg	acc	gat	caa	gac	624	
Lys	Gly	Tyr	Gly	Ser	Ile	Lys	Lys	Val	Tyr	Ile	Trp	Thr	Asp	Gln	Asp		
		195					200				205						
aaa	ata	ttc	ctg	ccg	gac	ttc	caa	cgc	tgg	caa	att	gca	aac	tac	aaa	672	
Lys	Ile	Phe	Leu	Pro	Asp	Phe	Gln	Arg	Trp	Gln	Ile	Ala	Asn	Tyr	Lys		
	210					215				220							
ccg	gac	aag	gtt	tat	cag	gtt	caa	ggc	ggc	gat	cac	aag	ctg	cag	ctg	720	
Pro	Asp	Lys	Val	Tyr	Gln	Val	Gln	Gly	Gly	Asp	His	Lys	Leu	Gln	Leu		

225 230 235 240

aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca 768
 Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala
 245 250 255~

tac gct taa 777
 Tyr Ala

<210> 30
 <211> 258
 <212> PRT
 <213> Manihot esculenta

<220>
 <223> Modified SHNL involving
 a replacement of Lys by Asn at position 21

<400> 30
 Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala
 1 5 10 15
 Trp Ile Trp His Asn Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys
 20 25 30
 Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile
 35 40 45
 Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe
 50 55 60
 Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser
 65 70 75 80
 Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys
 85 90 95
 Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His
 100 105 110
 Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp
 115 120 125
 Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile
 130 135 140
 Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr
 145 150 155 160
 Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys
 165 170 175
 Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu
 180 185 190
 Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp

195	200	205
Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys		
210	215	220
Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu		
225	230	235
Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala		
245	250	255
Tyr Ala		

<210> 31

<211> 777

<212> DNA

<213> Manihot esculenta

<220>

<221> CDS

<222> (1).. (777)

<220>

<223> cDNA coding for Modified SHNL involving
replacement of Gly by Glu at position 165 and Val by Leu at position 173

<400> 31

atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca	48
Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala	
1 5 10 15	

tgg att tgg cac aaa ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa	96
Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys	
20 25 30	

gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att	144
Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile	
35 40 45	

gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc	192
Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe	
50 55 60	

ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc	240
Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser	
65 70 75 80	

tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa 288
 Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys
 85 90 95

att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac 336
 Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His
 100 105 110

agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg 384
 Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp
 115 120 125

cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc 432
 Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile
 130 135 140

act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc acc 480
 Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr
 145 150 155 160

aaa tgc act gat gaa gaa tat gaa ctg gca aaa atg ctg atg cgc aag 528
 Lys Cys Thr Asp Glu Glu Tyr Glu Leu Ala Lys Met Leu Met Arg Lys
 165 170 175

ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa 576
 Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu
 180 185 190

aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac 624
 Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp
 195 200 205

aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa 672
 Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys
 210 215 220

ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg 720
 Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu
 225 230 235 240

aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca 768
 Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala
 245 250 255

tac gct taa 777

Tyr Ala

<210> 32

<211> 258

<212> PRT

<213> Manihot esculenta

<220>

<223> Modified SHNL involving

replacement of Gly by Glu at position 165 and Val by Leu at position 173

<400> 32

Met	Val	Thr	Ala	His	Phe	Val	Leu	Ile	His	Thr	Ile	Cys	His	Gly	Ala	1	5	10	15
Trp	Ile	Trp	His	Lys	Leu	Lys	Pro	Ala	Leu	Glu	Arg	Ala	Gly	His	Lys	20	25	30	
Val	Thr	Ala	Leu	Asp	Met	Ala	Ala	Ser	Gly	Ile	Asp	Pro	Arg	Gln	Ile	35	40	45	
Glu	Gln	Ile	Asn	Ser	Phe	Asp	Glu	Tyr	Ser	Glu	Pro	Leu	Leu	Thr	Phe	50	55	60	
Leu	Glu	Lys	Leu	Pro	Gln	Gly	Glu	Lys	Val	Ile	Ile	Val	Gly	Glu	Ser	65	70	75	80
Cys	Ala	Gly	Leu	Asn	Ile	Ala	Ile	Ala	Ala	Asp	Arg	Tyr	Val	Asp	Lys	85	90	95	
Ile	Ala	Ala	Gly	Val	Phe	His	Asn	Ser	Leu	Leu	Pro	Asp	Thr	Val	His	100	105	110	
Ser	Pro	Ser	Tyr	Thr	Val	Glu	Lys	Leu	Leu	Glu	Ser	Phe	Pro	Asp	Trp	115	120	125	
Arg	Asp	Thr	Glu	Tyr	Phe	Thr	Phe	Thr	Asn	Ile	Thr	Gly	Glu	Thr	Ile	130	135	140	
Thr	Thr	Met	Lys	Leu	Gly	Phe	Val	Leu	Leu	Arg	Glu	Asn	Leu	Phe	Thr	145	150	155	160
Lys	Cys	Thr	Asp	Glu	Glu	Tyr	Glu	Leu	Ala	Lys	Met	Leu	Met	Arg	Lys	165	170	175	
Gly	Ser	Leu	Phe	Gln	Asn	Val	Leu	Ala	Gln	Arg	Pro	Lys	Phe	Thr	Glu	180	185	190	
Lys	Gly	Tyr	Gly	Ser	Ile	Lys	Lys	Val	Tyr	Ile	Trp	Thr	Asp	Gln	Asp	195	200	205	
Lys	Ile	Phe	Leu	Pro	Asp	Phe	Gln	Arg	Trp	Gln	Ile	Ala	Asn	Tyr	Lys	210	215	220	
Pro	Asp	Lys	Val	Tyr	Gln	Val	Gln	Gly	Gly	Asp	His	Lys	Leu	Gln	Leu	225	230	235	240
Thr	Lys	Thr	Glu	Glu	Val	Ala	His	Ile	Leu	Gln	Glu	Val	Ala	Asp	Ala	245	250	255	

Tyr Ala

<210> 33

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 33

tatgaactgg caaaaatgct gctgcgcaag ggctctctgt tc

42

<210> 34

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 34

gaacagagag cccttgcgca gcagcatttt tgccagttca ta

42

<210> 35

<211> 777

<212> DNA

<213> Manihot esculenta

<220>

<221> CDS

<222> (1)..(777)

<220>

<223> cDNA coding for Modified SHNL involving

replacement of Gly by Glu at position 165 and Val by Leu at position 173
and Met by Leu at position 174

<400> 35

atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca
Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala

48

36/49

aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac 624
 Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp
 195 200 205

aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa 672
 Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys
 210 215 220

ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg 720
 Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu
 225 230 235 240

aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca 768
 Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala
 245 250 255

tac gct taa 777
 Tyr Ala

<210> 36
 <211> 258
 <212> PRT
 <213> Manihot esculenta

<220>
 <223> Modified SHNL involving
 replacement of Gly by Glu at position 165 and Val by Leu at position 173
 and Met by Leu at position 174

<400> 36
 Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala
 1 5 10 15
 Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys
 20 25 30
 Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile
 35 40 45
 Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe
 50 55 60
 Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser
 65 70 75 80
 Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys
 85 90 95
 Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His

	100		105		110										
Ser	Pro	Ser	Tyr	Thr	Val	Glu	Lys	Leu	Leu	Glu	Ser	Phe	Pro	Asp	Trp
	115		120		125										
Arg	Asp	Thr	Glu	Tyr	Phe	Thr	Phe	Thr	Asn	Ile	Thr	Gly	Glu	Thr	Ile
	130		135		140										
Thr	Thr	Met	Lys	Leu	Gly	Phe	Val	Leu	Leu	Arg	Glu	Asn	Leu	Phe	Thr
	145		150		155										
Lys	Cys	Thr	Asp	Glu	Glu	Tyr	Glu	Leu	Ala	Lys	Met	Leu	Leu	Arg	Lys
	165		170		175										
Gly	Ser	Leu	Phe	Gln	Asn	Val	Leu	Ala	Gln	Arg	Pro	Lys	Phe	Thr	Glu
	180		185		190										
Lys	Gly	Tyr	Gly	Ser	Ile	Lys	Lys	Val	Tyr	Ile	Trp	Thr	Asp	Gln	Asp
	195		200		205										
Lys	Ile	Phe	Leu	Pro	Asp	Phe	Gln	Arg	Trp	Gln	Ile	Ala	Asn	Tyr	Lys
	210		215		220										
Pro	Asp	Lys	Val	Tyr	Gln	Val	Gln	Gly	Gly	Asp	His	Lys	Leu	Gln	Leu
	225		230		235										
Thr	Lys	Thr	Glu	Glu	Val	Ala	His	Ile	Leu	Gln	Glu	Val	Ala	Asp	Ala
	245		250		255										
Tyr	Ala														

<210> 37

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 37

tgaaaacctg ttcaccaaatt gccnnngatgg cgaatatgaa ctggc

45

<210> 38

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 38

gccagttcat attcgccatc nnngcatttg gtgaacaggt tttca

45

<210> 39
 <211> 777
 <212> DNA
 <213> Manihot esculenta

<220>
 <223> cDNA coding for Modified SHNL involving
 a replacement of Thr by Asp at position 163

<220>
 <221> CDS
 <222> (1)..(777)
 <223>

<400> 39
 atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca 48
 Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala
 1 5 10 15
 tgg att tgg cac aaa ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa 96
 Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys
 20 25 30
 gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att 144
 Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile
 35 40 45
 gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc 192
 Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe
 50 55 60
 ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc 240
 Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser
 65 70 75 80
 tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa 288
 Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys
 85 90 95
 att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac 336
 Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His
 100 105 110
 agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg 384

Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp
 115 120 125
 cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc 432
 Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr-Ile
 130 135 140
 act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc acc 480
 Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr
 145 150 155 160
 aaa tgc gat gat ggc gaa tat gaa ctg gca aaa atg gtt atg cgc aag 528
 Lys Cys Asp Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys
 165 170 175
 ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa 576
 Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu
 180 185 190
 aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac 624
 Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp
 195 200 205
 aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa 672
 Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys
 210 215 220
 ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg 720
 Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu
 225 230 235 240
 aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca 768
 Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala
 245 250 255
 tac gct taa 777
 Tyr Ala

<210> 40
 <211> 258
 <212> PRT
 <213> Manihot esculenta

<220>

<223> Modified SHNL involving
a replacement of Thr by Asp at position 163

<400> 40

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala
1 5 10 15

Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys
20 25 30

Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile
35 40 45

Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe
50 55 60

Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser
65 70 75 80

Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys
85 90 95

Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His
100 105 110

Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp
115 120 125

Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile
130 135 140

Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr
145 150 155 160

Lys Cys Asp Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys
 165 170 175

Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu
 180 185 190

Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp
 195 200 205

Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys
 210 215 220

Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu
 225 230 235 240

Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala
 245 250 255

Tyr Ala

<210> 41

<211> 777

<212> DNA

<213> Manihot esculenta

<220>

<223> cDNA coding for Modified SHNL involving
 a replacement of Thr by Glu at position 163

<220>

<221> CDS

<222> (1).. (777)

<223>

<400> 41

atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca 48

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala
 1 5 10 15

tgg att tgg cac aaa ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa 96
 Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys
 20 25 30

gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att 144
 Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile
 35 40 45

gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc 192
 Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe
 50 55 60

ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc 240
 Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser
 65 70 75 80

tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa 288
 Cys Ala Gly Leu Asn Ile Ala Ile Ala Asp Arg Tyr Val Asp Lys
 85 90 95

att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac 336
 Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His
 100 105 110

agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg 384
 Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp
 115 120 125

cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc 432
 Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile
 130 135 140

act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc acc 480
 Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr
 145 150 155 160

aaa tgc gaa gat ggc gaa tat gaa ctg gca aaa atg gtt atg cgc aag 528
 Lys Cys Glu Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys
 165 170 175

ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa 576
 Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu

Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile
35 40 45

Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe
50 55 60

Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser
65 70 75 80

Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys
85 90 95

Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His
100 105 110

Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp
115 120 125

Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile
130 135 140

Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr
145 150 155 160

Lys Cys Glu Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys
165 170 175

Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu
180 185 190

Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp
195 200 205

Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys
210 215 220

Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu
 225 230 235 240

Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp-Ala
 245 250 255

Tyr Ala

<210> 43

<211> 777

<212> DNA

<213> Manihot esculenta

<220>

<223> cDNA coding for Modified SHNL involving
 a replacement of Thr by Ser at position 163

<220>

<221> CDS

<222> (1)..(777)

<223>

<400> 43

atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca 48
 Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala
 1 5 10 15

tgg att tgg cac aaa ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa 96
 Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys
 20 25 30

gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att 144
 Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile
 35 40 45

gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc 192
 Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe
 50 55 60

ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc 240
 Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser

65	70	75	80	
tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa				288
Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys				
	85	90	95 -	
att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac				336
Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His				
	100	105	110	
agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg				384
Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp				
	115	120	125	
cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc				432
Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile				
	130	135	140	
act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc acc				480
Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr				
	145	150	155	160
aaa tgc tct gat ggc gaa tat gaa ctg gca aaa atg gtt atg cgc aag				528
Lys Cys Ser Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys				
	165	170	175	
ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa				576
Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu				
	180	185	190	
aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac				624
Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp				
	195	200	205	
aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa				672
Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys				
	210	215	220	
ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg				720
Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu				
	225	230	235	240
aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca				768
Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala				
	245	250	255	

tac gct taa
Tyr Ala

777

<210> 44
<211> 258
<212> PRT
<213> Manihot esculenta

<220>

<223> Modified SHNL involving
a replacement of Thr by Ser at position 163

<400> 44

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala
1 5 10 15

Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys
20 25 30

Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile
35 40 45

Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe
50 55 60

Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser
65 70 75 80

Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys
85 90 95

Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His
100 105 110

Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp
115 120 125

Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile
130 135 140

Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr
145 150 155 160

Lys Cys Ser Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys
165 170 175

Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu
180 185 190

Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp
195 200 205

Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys
210 215 220

Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu
225 230 235 240

Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala
245 250 255

Tyr Ala